

data flow between the cPCI bus on the one hand and the transmitter and receiver on the other hand once the free-space optical link has been established. The data rates in transmission and reception need not be equal and could even differ by as much as several orders of magnitude. The data relay board would contain a commercially available network processor programmed to perform the primitive data handling function required by the protocol. Using a memory buffer, the network processor would accept, from the user application or storage through the cPCI bus, a stream of data to be transmitted to the laser. The network processor would form the data into appropriately sized frames with headers and frame sequence information to identify frames for the ARQ process. The frames would then be sent to an interface adaptor for frame acquisition and synchronization.

The interface adaptor would then format the data into 16-bit words, add error check bits, and send the data to the serializer and encoder for transmission to the laser.

As successful receipt of frames is acknowledged using the free-space optical link in the reverse direction, the corresponding data are cleared from the local memory so that capacity for new streaming data is made available. In the event of missed or corrupted data frames, the network processor will reconstruct and retransmit the data frames over the free-space optical link.

On the receiving side, the interface adapter will check for errors, while the network processor will check for frames out of sequence. For each received frame, the network processor will generate the appropriate ARQ control frame and pass it to the reverse channel

free-space optical-link interface for transmission.

This work was done by Malcolm Wright and Loren Clare of Caltech and Gary Gould and Maxim Pedyash of Rockwell Scientific Center for NASA's Jet Propulsion Laboratory. Further information is contained in a TSP (see page 1).

In accordance with Public Law 96-517, the contractor has elected to retain title to this invention. Inquiries concerning rights for its commercial use should be addressed to

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Refer to NPO-30610, volume and number of this NASA Tech Briefs issue, and the page number.

Software and Algorithms for Biomedical Image Data Processing and Visualization

PlaqTrak automatically assesses plaque deposits on teeth.

NASA's Jet Propulsion Laboratory, Pasadena, California

A new software equipped with novel image processing algorithms and graphical-user-interface (GUI) tools has been designed for automated analysis and processing of large amounts of biomedical image data. The software, called PlaqTrak, has been specifically used for analysis of plaque on teeth of patients.

New algorithms have been developed and implemented to segment teeth of interest from surrounding gum, and a real-time image-based morphing procedure is used to automatically overlay a grid onto each segmented tooth. Pattern recognition

methods are used to classify plaque from surrounding gum and enamel, while ignoring glare effects due to the reflection of camera light and ambient light from enamel regions. The PlaqTrak system integrates these components into a single software suite with an easy-to-use

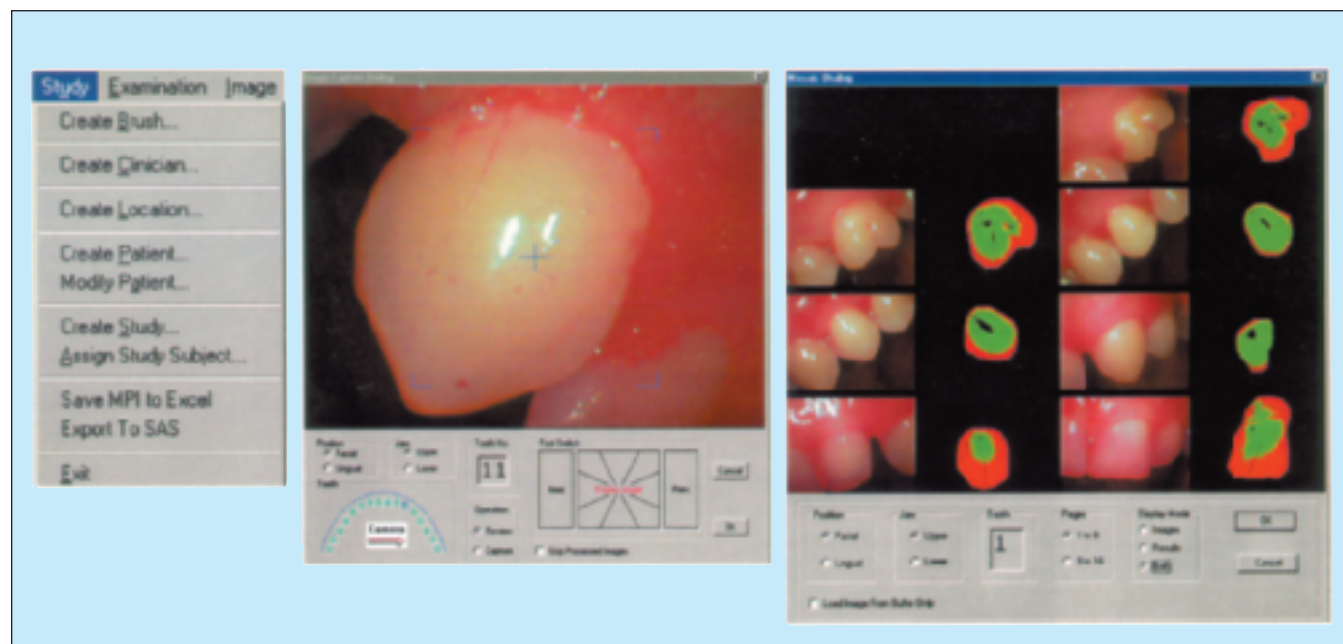


Figure 1. PlaqTrak System Utilities are showing some of the GUI tools.

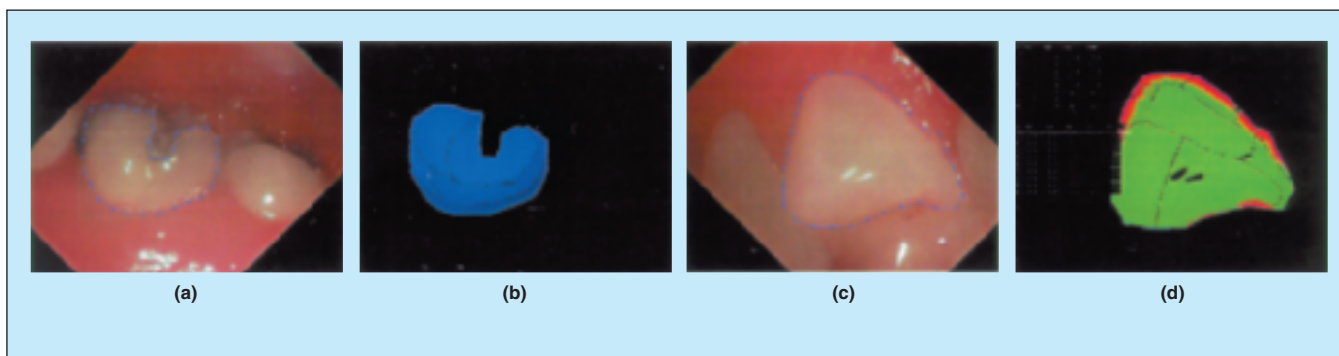


Figure 2. Examples are shown of **Biomedical Image** segmentation, morphing, and classification.

GUI (see Figure 1) that allows users to do an end-to-end run of a patient's record, including tooth segmentation of all teeth, grid morphing of each segmented tooth, and plaque classification of each tooth image.

The automated and accurate processing of the captured images to segment each tooth [see Figure 2(a)] and then detect plaque on a tooth-by-tooth basis is a critical component of the PlaqTrak system to do clinical trials and analysis with minimal human intervention. These features offer distinct advantages over other competing systems that analyze groups of teeth or synthetic teeth. PlaqTrak divides each segmented tooth into eight regions

using an advanced graphics morphing procedure [see results on a chipped tooth in Figure 2(b)], and a pattern recognition classifier is then used to locate plaque [red regions in Figure 2(d)] and enamel regions. The morphing allows analysis within regions of teeth, thereby facilitating detailed statistical analysis such as the amount of plaque present on the biting surfaces on teeth.

This software system is applicable to a host of biomedical applications, such as cell analysis and life detection, or robotic applications, such as product inspection or assembly of parts in space and industry.

This work was done by Ashit Talukder, James Lambert, and Raymond Lam of Cal-

tech for NASA's Jet Propulsion Laboratory. Further information is contained in a TSP (see page 1).

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Rapid Chemometric Filtering of Spectral Data

Target species would be identified in real time.

NASA's Jet Propulsion Laboratory, Pasadena, California

A method of rapid, programmable filtering of spectral transmittance, reflectance, or fluorescence data to measure the concentrations of chemical species has been proposed. By "programmable" is meant that a variety of spectral analyses can readily be performed and modified in software, firmware, and/or electronic hardware, without need to change optical filters or other optical hardware of the associated spectrometers. The method is intended to enable real-time identification of single or multiple target chemical species in applications that involve high-throughput screening of multiple samples. Examples of such applications include (but are not limited to) combinatorial chemistry, flow cytometry, bead assays, testing drugs, remote sensing, and identification of targets.

The basic concept of the proposed method is to perform real-time cross-

correlations of a measured spectrum with one or more analytical function(s) of wavelength that could be, for example, the known spectra of target species. Assuming that measured spectral intensities are proportional to concentrations of target species plus background spectral intensities, then after subtraction of background levels, it should be possible to determine target-species concentrations from cross-correlation values. Of course, the problem of determining the concentrations is more complex when spectra of different species overlap, but the problem can be solved by use of multiple analytical functions in combination with computational techniques that have been developed previously for analyses of this type.

The method is applicable to the design and operation of a spectrometer in which spectrally dispersed light is mea-

sured by means of an active-pixel sensor (APS) array. The row or column dimension of such an array is generally chosen to be aligned along the spectral-dispersion dimension, so that each pixel intercepts light in a narrow spectral band centered on a wavelength that is a known function of the pixel position. The proposed method admits of two hardware implementations for computing cross-correlations in real time.

One hardware implementation would exploit programmable circuitry within each pixel of an APS array. The analog spectral-intensity reading of the photodetector in each pixel would be multiplied by a gain proportional to value of the analytical function for the wavelength that corresponds to the pixel position. As a result, the output from each pixel would be proportional to contribution of the pixel to the cross-correlation (plus background). The outputs of